

Amendments to the Claims under 37 C.F.R. § 1.121

Claims 1-7 (cancelled).

Claim 8 (currently amended): A method for detecting human papilloma virus (HPV) DNA in a cell sample which indicates the patient providing the cell sample is at risk for cancer, comprising:

(a) adding a reagent comprising a plurality of genomic HPV DNA probe sets to the cell sample under suitable hybridization conditions, wherein:

(i) a first genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments ~~having different nucleotide sequences prepared by labeling essentially the full-length genomic sequence of HPV type 16 that detectably hybridize to a plurality of different nucleotide sequences of essentially the full-length genomic sequence of HPV type 16,~~

(ii) a second genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments ~~having different nucleotide sequences prepared by labeling essentially the full-length genomic sequence of HPV type 18 that detectably hybridize to a plurality of different nucleotide sequences of essentially the full-length genomic sequence of HPV type 18,~~

(iii) a third genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments ~~having different nucleotide sequences prepared by labeling essentially the full-length genomic sequence of HPV type 31 that detectably hybridize to a plurality of different nucleotide sequences of essentially the full-length genomic sequence of HPV type 31,~~

(iv) a fourth genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments ~~having different nucleotide sequences prepared by labeling essentially the full-length genomic sequence of HPV type 33 that detectably hybridize to a plurality of different nucleotide sequences of essentially the full-length genomic sequence of HPV type 33,~~

(v) a fifth genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments ~~having different nucleotide sequences prepared by labeling essentially the full-length genomic sequence of HPV type 35 that detectably hybridize to a plurality of different nucleotide sequences of essentially the full-length genomic sequence of HPV type 35,~~ and

(vi) a sixth genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments ~~having different nucleotide sequences prepared by labeling essentially the full-length genomic sequence of HPV type 51 that detectably hybridize to a plurality of different nucleotide sequences of essentially the full-length genomic sequence of HPV type 51;~~

wherein the labeled nucleic acid fragments of the genomic HPV DNA probe sets detectably hybridize to the genomic sequence of HPV types 39, 45, 52, 56, 58, 59, 68 and 70 in addition to detectably hybridizing to the genomic sequence of HPV types 16, 18, 31, 33, 35, and 51; and

~~and wherein the~~ labeled nucleic acid fragments of the genomic HPV DNA probe sets do not detectably hybridize to the genomic sequence of ~~a low-risk HPV types 42, 43, or 44;~~ and

(b) determining whether the labeled nucleic acid fragments of the genomic HPV DNA probe sets detectably hybridize to HPV DNA in the cell sample.

Claim 9 (currently amended): The method of claim 8, wherein the proportion of total HPV DNA in the reagent that comprises labeled nucleic acid fragments of the first genomic HPV DNA probe set and the proportion of total HPV DNA in the reagent that comprises labeled nucleic acid fragments of the third genomic HPV DNA probe set are decreased relative to the proportions of the total HPV DNA in the reagent that comprise labeled nucleic acid fragments of the other HPV DNA probe sets.

Claim 10 (currently amended): The method of claim 8, wherein ~~the reagent is hybridized to the cell sample~~ hybridization conditions comprise washing the cell sample at 45°C in a buffer

comprising 2X SSC and 2% BSA.

Claim 11 (previously presented): The method of claim 8, further comprising pretreating the cell sample with a protease.

Claim 12 (previously presented): The method of claim 8, further comprising destaining and/or deparaffining the cell sample.

Claims 13-14 (cancelled).

Claim 15 (currently amended): The method of claim 8, wherein:

- (a) the plurality of labeled nucleic acid fragments of the first genomic HPV DNA probe set constitute about 8.3% of the total HPV DNA in the reagent,
- (b) the plurality of labeled nucleic acid fragments of the second genomic HPV DNA probe set constitute about 20.8% of the total HPV DNA in the reagent,
- (c) the plurality of labeled nucleic acid fragments of the third genomic HPV DNA probe set constitute about 8.3% of the total HPV DNA in the reagent,
- (d) the plurality of labeled nucleic acid fragments of the fourth genomic HPV DNA probe set constitute about 20.8% of the total HPV DNA in the reagent,
- (e) the plurality of labeled nucleic acid fragments of the fifth genomic HPV DNA probe set constitute about 20.8% of the total HPV DNA in the reagent, and
- (f) the plurality of labeled nucleic acid fragments of the sixth genomic HPV DNA probe set constitute about 20.8% of the total HPV DNA in the reagent.

Claim 16 (previously presented): The method of claim 8, wherein the cell sample contains abnormal cervical cells.

Claims 17-22 (cancelled).

Claim 23 (new): The method of claim 8, wherein the plurality of labeled nucleic acid fragments of the genomic HPV DNA probe sets are labeled by nick translation.

Claim 24 (new): The method of claim 8, wherein the plurality of labeled nucleic acid fragments of the genomic HPV DNA probe sets are labeled by polymerase chain reaction (PCR).

Claim 25 (new): The method of claim 8, wherein the plurality of labeled nucleic acid fragments of the genomic HPV DNA probe sets are labeled by random priming.